

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☒ 7. Seq ID 5 is Reversed Polarity
Other: _____

Applicant must provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/423,194DATE: 11/29/95
TIME: 15:11:35

INPUT SET: S7583.raw

#3
MB
12/01/95

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Eaton, Dan L.
de Sauvage, Frederic J.

(ii) TITLE OF INVENTION: MPL LIGAND

(iii) NUMBER OF SEQUENCES: 77

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: patin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/423194
(B) FILING DATE: 18-APR-1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/249376
(B) FILING DATE: 25-MAY-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/223263
(B) FILING DATE: 04-APR-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/196689
(B) FILING DATE: 15-FEB-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994

ENTERED

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/423,194DATE: 11/29/95
TIME: 15:11:39

INPUT SET: S7583.raw

47 (vii) PRIOR APPLICATION DATA:
48 (A) APPLICATION NUMBER: 08/176553
49 (B) FILING DATE: 03-JAN-1994
50
51 (viii) ATTORNEY/AGENT INFORMATION:
52 (A) NAME: Winter, Daryl B.
53 (B) REGISTRATION NUMBER: 32,637
54 (C) REFERENCE/DOCKET NUMBER: 871P4D2
55
56 (ix) TELECOMMUNICATION INFORMATION:
57 (A) TELEPHONE: 415/225-1249
58 (B) TELEFAX: 415/952-9881
59 (C) TELEX: 910/371-7168
60
61 (2) INFORMATION FOR SEQ ID NO:1:
62
63 (i) SEQUENCE CHARACTERISTICS:
64 (A) LENGTH: 353 amino acids
65 (B) TYPE: amino acid
66 (D) TOPOLOGY: linear
67
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
69
70 Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
71 -21 -20 -15 -10
72
73 Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
74 -5 1 5
75
76 Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
77 10 15 20
78
79 Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
80 25 30 35
81
82 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
83 40 45 50
84
85 Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
86 55 60 65
87
88 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
89 70 75 80
90
91 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
92 85 90 95
93
94 Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
95 100 105 110
96
97 Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
98 115 120 125
99

RAW SEQUENCE LISTING PATENT APPLICATION US/08/423,194

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100 Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
101 130                      135                      140
102
103 Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
104 145                      150                      155
105
106 Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
107 160                      165                      170
108
109 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
110 175                      180                      185
111
112 Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
113 190                      195                      200
114
115 Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
116 205                      210                      215
117
118 Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
119 220                      225                      230
120
121 Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
122 235                      240                      245
123
124 Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
125 250                      255                      260
126
127 Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
128 265                      270                      275
129
130 Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
131 280                      285                      290
132
133 Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
134 295                      300                      305
135
136 Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
137 310                      315                      320
138
139 Ser Gln Asn Leu Ser Gln Glu Gly
140 325                      330                      332
141

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/423,194DATE: 11/29/95
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153 TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50
154
155
156 CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100
157
158
159 CCCCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150
160
161
162 CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200
163
164
165 GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250
166
167
168 TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300
169
170
171 ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350
172
173
174 AGACTGAGCC AGTGCCGAGA GGTTCACCCT TTGCCTACAC CTGTCCTGCT 400
175
176
177 GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450
178
179
180 CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500
181
182
183 ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550
184
185
186 GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600
187
188
189 TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650
190
191
192 AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700
193
194
195 CCTGATGCTT GTAGGAGGGT CCACCCTCTG CGTCAGGCGG GCCCCACCCA 750
196
197
198 CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800
199
200
201 CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850
202
203
204 AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAGA 900
205

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/423,194DATE: 11/29/95
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206
207 TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950
208
209
210 TACCTGAACA GGATACACGA ACTCTTGAAT GGAACCTCGTG GACTCTTTCC 1000
211
212
213 TGGACCCCTCA CGCAGGACCC TAGGAGCCCC GGACATTTCC TCAGGAACAT 1050
214
215
216 CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100
217
218
219 CCAACCCATC CTCCTACTGG ACAGTATACG CTCTTCCCTC TTCCACCCAC 1150
220
221
222 CTTGCCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200
223
224
225 CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250
226
227
228 TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300
229
230
231 AGCATTTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350
232
233
234 AACTGGACAA GATTTCTTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400
235
236
237 GGGATACACA GGAAGTAAAA GGGAAATCATT TTTCACCTGA CATTATAAAC 1450
238
239
240 CTTCAGAAGC TATTTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500
241
242
243 GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG ATTCTCTACA 1550
244
245
246 TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600
247
248
249 GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650
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251
252 TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCATCC CCTTTACTAT 1700
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254
255 CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC TTTACTCTTG 1750
256
257
258 AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA AAAAA 1795

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/423,194

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Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/423194